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Entry information

Entry name	SPB7_HUMAN
Primary accession number	O75635
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 41, February 2003
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	Megsin
Synonyms	TP55 — Serpin B7
Gene name	SERPINB7
From	Homo sapiens (Human) [TaxID: 9606]
Taxonomy	Eukaryota ; Metazoa ; Chordata ; Craniata ; Vertebrata ; Euteleostomi ; Mammalia ; Eutheria ; Primates ; Catarrhini ; Hominidae ; Homo .

References

[1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=97326116; PubMed=9182567; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Tsujimoto M.](#), [Tsunuoka N.](#), [Ishida N.](#), [Kurihara T.](#), [Iwasa F.](#), [Yamashiro K.](#), [Rogi T.](#), [Kodama S.](#), [Katsuragi N.](#), [Adachi M.](#), [Katayama T.](#), [Nakao M.](#), [Yamaichi K.](#), [Hashino J.](#), [Haruyama M.](#), [Miura K.](#), [Nakanishi T.](#), [Nakazato H.](#), [Teramura M.](#), [Mizoguchi H.](#), [Yamaguchi N.](#);

"Purification, cDNA cloning, and characterization of a new serpin with megakaryocyte maturation activity.";

J. Biol. Chem. 272:15373-15380(1997).

[2] SEQUENCE FROM NUCLEIC ACID.

TISSUE=[Mesangial cells](#);

MEDLINE=98376492; PubMed=9710452; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]

[Miyata T.](#), [Nangaku M.](#), [Suzuki D.](#), [Inagi R.](#), [Uragami K.](#), [Sakai H.](#), [Okubo K.](#), [Kurokawa K.](#);

"A mesangium-predominant gene, megsin, is a new serpin upregulated in IgA nephropathy.";

J. Clin. Invest. 102:828-836(1998).

Comments

- **FUNCTION:** Might function as an inhibitor of Lys-specific proteases. Might influence the maturation of megakaryocytes via its action as a serpin.
- **SUBCELLULAR LOCATION:** Cytoplasmic (*By similarity*).
- **TISSUE SPECIFICITY:** Predominantly expressed in mesangial cells.
- **SIMILARITY:** Belongs to the serpin family. Ov-serpin subfamily.

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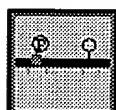
Cross-references

EMBL	D88575; BAA31232.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence] AF027866; AAC64506.1; -. [EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P05619 ; 1HLE. [HSSP ENTRY / PDB]
Genew	HGNC:13902 ; SERPINB7.
CleanEx	HGNC:13902 ; SERPINB7.
GeneCards	SERPINB7 .
GeneLynx	SERPINB7 ; Homo sapiens.
GenAtlas	SERPINB7 .
MIM	603357 [NCBI / EBI].
GO	GO:0004868 ; Molecular function: serpin (<i>traceable author statement</i>).
SOURCE	SERPINB7 ; Homo sapiens.
Ensembl	O75635; Homo sapiens. [Entry / Contig view]
InterPro	IPR000215 ; Serpin. Graphical view of domain structure .
Pfam	PF00079 ; serpin; 1.
SMART	SM00093 ; SERPIN; 1.
PROSITE	PS00284 ; SERPIN; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]
HOVERGEN	[Family / Alignment / Tree]
BLOCKS	O75635 .
ProtoNet	O75635 .
ProtoMap	O75635 .
PRESAGE	O75635 .
DIP	O75635 .
ModBase	O75635 .
SMR	O75635 ; 9A2CDB6C63CFF605.
SWISS-2DPAGE	Get region on 2D PAGE .

Keywords

[Serpins](#); [Serine protease inhibitor](#).

Features



[Feature table viewer](#)

Key	From	To	Length	Description
ACT_SITE	347	348		REACTIVE BOND (BY SIMILARITY).

Sequence information

Length: 380 Molecular weight: 42904 CRC64: 9A2CDB6C63CFF605 [This is a checksum on the AA sequence]

10	20	30	40	50	60
MASLAAANAE	FCFNLFREMD	DNQGNGNVFF	SSLSLFAALA	LVRLGAQDD	LSQIDKLLHV
70	80	90	100	110	120
NTASGYGNSS	NSQSQLQSQL	KRVFSDINAS	HKDYDLSIVN	GLFAEKVYGF	HKDYIECAEK
130	140	150	160	170	180
LYDAKVERVD	FTNHLEDTRR	NINKWVENET	HGKIKNVIGE	GGISSLSSAVMV	LVNAVYFKGK
190	200	210	220	230	240
WQSAFTKSET	INCHFKSPKC	SGKAVAMMHO	ERKFNLSVIE	DPSMKILELR	YNGGINMYVL
250	260	270	280	290	300
LPENDLSEIE	NKLTQNLME	WTNPQRRMTSK	YVEVFFPQFK	IEKNYEMKQY	LRALGLKDIF
310	320	330	340	350	360
DESKADLSGI	ASGGRLYISR	MMHKSYIEVT	EEGTEATAAT	GSNIVEKQLP	QSTLFRADHP
370	380				
FLFVIRKDDI	ILFSGKVSCP				

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[Dotlet](#) (Java)



[ScanProsite](#), [MotifScan](#)



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